

**IN THE CLAIMS:**

Claims 1 and 13 are amended herein and new claim 18 is presented. Please note that all claims currently pending in the referenced application are shown below. Please enter these claims as amended. Upon entry, this listing of claims will replace all prior versions and listings of claims in the application.

**Listing of Claims:**

1. (Currently Amended) A process of identifying transcription factors such as activators and/or repressors comprising:

providing cells with a nucleic acid sequence at least comprising a sequence CACCT (SEQ ID NO: 1) , ~~preferably twice a CACCT sequence (SEQ ID NO: 1),~~ as bait(s) bait for the screening of a library encoding potential transcription factors and performing a specificity test to isolate said transcription factors.

2. (Previously Presented) A process of identifying transcription factors such as activators and/or repressors comprising:

providing cells with a nucleic acid sequence comprising one of the sequences CACCT-N-CACCT (a first SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), or AGGTG-N-AGGTG (a first SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N) as bait wherein N is a spacer sequence.

3. (Original) A process according to claim 1 wherein the transcription factor comprises separated clusters of zinc fingers.

4. (Original) A process according to claim 1 wherein the sequence originates from a

promoter region.

5. (Original) A process according to claim 4 wherein the promoter region is selected from the group consisting of Brachyury,  $\alpha$ 4-integrin, follistatin, and E-cadherin.

6. (Original) A transcription factor produced by the process of claim 1.

7. (Previously Presented) A process for identifying compounds with an interference capability towards transcription factors as defined in claim 6 by adding a sample comprising a potential compound to be identified to a test system comprising: (i) a nucleotide sequence comprising one of the sequences CACCT-N-CACCT (a first\_SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), or AGGTG-N-AGGTG (a first SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N) as bait wherein N is a spacer, and (ii) a protein capable to bind said nucleotide sequence, incubating said sample in said system for a period of time sufficient to permit interaction of the compound or its derivative or counterpart thereof with said protein, comparing the amount and/or activity of the protein bound to the nucleotide sequence before and after said adding and identification and optionally isolation and/or purification of the compound.

8. (Original) The process according to claim 7 wherein the protein is a Smad-interacting protein.

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9. (Original) The process according to claim 8, wherein said Smad-interacting protein is SIP1.

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10. (Original) A compound produced by the process of claim 7.

11. (Original) The compound of claim 10, wherein said compound modifies regulation of E-cadherin expression by SIP1.

12. (Original) A pharmaceutical composition to prevent tumor invasion and/or metastasis, said pharmaceutical composition comprising:  
the compound of claim 10 in an amount to prevent tumor invasion and/or metastasis in a subject,  
and  
a pharmaceutically acceptable excipient.

13. (Currently Amended) A test kit to perform the process of claim 7, said test kit comprising:  
a nucleotide sequence comprising a sequence selected from the group consisting of CACCT-N-CACCT (a first SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), and AGGTG-N-AGGTG (a first SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N), wherein N is a spacer sequence and  
(ii) a protein capable of binding said nucleotide sequence.

14. (Previously Presented) A test kit to perform the process of claim 2, said test kit comprising:  
a nucleic acid sequence comprising one of the sequences CACCT-N-CACCT (a first SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), or AGGTG-N-AGGTG (a first SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N), wherein N is a spacer sequence.

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15. (Previously Presented) A method for detecting an interaction between a first interacting protein and a second interacting protein comprising:

providing a suitable host cell with a first fusion protein comprising a first interacting protein fused to a DNA binding domain capable to bind a nucleic acid sequence comprising one of the sequences CACCT-N-CACCT (a first\_SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), or AGGTG-N-AGGTG (a first SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N), wherein N is a spacer sequence,

providing said suitable host cell with a second fusion protein comprising a second interacting protein fused to a DNA binding domain capable to bind a nucleic acid sequence comprising one of the sequences CACCT-N-CACCT (a first\_SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), or AGGTG-N-AGGTG (a first\_SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N), wherein N is a spacer sequence,

subjecting said host cell to conditions under which the first interacting protein and the second interacting protein are brought into close proximity and determining whether a detectable gene present in the host cell and located adjacent to said nucleic acid sequence has been expressed to a greater degree than if expressed in the absence of the interaction between the first and the second interacting protein.

16. (Previously Presented) An isolated nucleic acid sequence comprising a sequence selected from the group consisting of CACCT-N-CACCT (a first SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), and AGGTG-N-AGGTG (a first\_SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N), wherein N is a spacer.

17. (Previously Presented) A method of identifying a new target gene, said method comprising:

identifying said new target gene using a nucleic acid sequence, said nucleic acid sequence comprising a sequence selected from the group consisting of CACCT (SEQ ID NO: 1), CACCT-N-CACCT (a first\_SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), or AGGTG-N-AGGTG (a first SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N), wherein N is a spacer.

18. (New) A process of identifying transcription factors such as activators and/or repressors comprising:

providing cells with a nucleic acid sequence at least comprising twice a CACCT sequence (SEQ ID NO: 1) as bait for the screening of a library encoding potential transcription factors, wherein the at least twice a sequence is selected from the group consisting of CACCT-N-CACCT (a first SEQ ID NO: 1 and a second SEQ ID NO:1 separated by N), CACCT-N-AGGTG (SEQ ID NO: 1 and SEQ ID NO:3 separated by N), AGGTG-N-CACCT (SEQ ID NO: 3 and SEQ ID NO:1 separated by N), and AGGTG-N-AGGTG (a first SEQ ID NO: 3 and a second SEQ ID NO:3 separated by N), wherein N is a spacer sequence.